```
FILE 'REGISTRY' ENTERED AT 10:53:46 ON 23 FEB 2006

=> S ENDONUCLEASE/CN
L1             1 ENDONUCLEASE/CN

=> D

L1   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   9055-11-2  REGISTRY
ED   Entered STN:  16 Nov 1984
CN   Nuclease, endo- (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   Cobra venom endonuclease
CN   Endonuclease
MF   Unspecified
CI   MAN
LC   STN Files:   ADISNEWS, AGRICOLA, BIOSIS, BIOTECHNO, CA, CAPLUS, CIN,
       CSCHEM, EMBASE, PROMT, TOXCENTER, USPAT2, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
            1562 REFERENCES IN FILE CA (1907 TO DATE)
              21 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
            1569 REFERENCES IN FILE CAPLUS (1907 TO DATE)


=> S NUCLEASE/CN
L2             1 NUCLEASE/CN

=> D

L2   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   9026-81-7  REGISTRY
ED   Entered STN:  16 Nov 1984
CN   Nuclease (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   Nucleic acid hydrolase
MF   Unspecified
CI   MAN
LC   STN Files:   ADISNEWS, AGRICOLA, BIOSIS, BIOTECHNO, CA, CAPLUS,
CASREACT,
       CHEMCATS, CIN, CSCHEM, EMBASE, IFICDB, IFIPAT, IFIUDB, NAPRALERT,
PROMT,
       TOXCENTER, USPAT2, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
            2589 REFERENCES IN FILE CA (1907 TO DATE)
              66 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
            2592 REFERENCES IN FILE CAPLUS (1907 TO DATE)

FILE 'CAPLUS' ENTERED AT 10:54:15 ON 23 FEB 2006

=> S ENDONUCLEASE;S NUCLEASE;S L1,L3;S L2,L4
         27561 ENDONUCLEASE
          8226 ENDONUCLEASES
L3       31976 ENDONUCLEASE
                (ENDONUCLEASE OR ENDONUCLEASES)
```

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          20902 NUCLEASE
           6307 NUCLEASES
L4        25079 NUCLEASE
                (NUCLEASE OR NUCLEASES)


           1569 L1
L5        32030 (L1 OR L3)


           2592 L2
L6        25157 (L2 OR L4)

=> S CEL I;S CEL II
           2294 CEL
            165 CELS
           2428 CEL
                (CEL OR CELS)
        4161362 I
L7           54 CEL I
                (CEL(W)I)


           2294 CEL
            165 CELS
           2428 CEL
                (CEL OR CELS)
        2069105 II
            895 IIS
        2069615 II
                (II OR IIS)
L8           21 CEL II
                (CEL(W)II)

=> S CELERY
           3305 CELERY
              3 CELERIES
L9         3307 CELERY
                (CELERY OR CELERIES)

=> S L9 AND L5
L10          14 L9 AND L5

=> S L9 AND L6
L11          10 L9 AND L6

=> S L10,L11
L12          17 (L10 OR L11)

=> D 1-17 CBIB ABS

L12  ANSWER 1 OF 17  CAPLUS  COPYRIGHT 2006 ACS on STN
2006:54886   Document No. 144:145421  Cloning, purification and sequence of
DNA
     mismatch-specific endonuclease CELII from celery.
     Shandilya, Harini; Gerard, Gary F.; Qui, Peter (Transgenomic, Inc.,
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USA).
PCT Int. Appl. WO 2006007124 A2 20060119, 59 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IS, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2005-US17508 20050518. PRIORITY: US 2004-2004/PV580450 20040617.

AB The present invention relates to isolated cDNA sequences encoding CELII DNA mismatch-specific **endonuclease** from **celery** and vectors and host cells for producing a protein encoded thereby. A modified purification method was developed that separated CELI and CELII **endonucleases.** The cDNA sequence and the encoded amino acid sequence of CELII from **celery** are disclosed.

L12 ANSWER 2 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN

2005:1355046 Document No. 144:47223 Molecular cloning and characterization of a cDNA encoding **endonuclease** from potato (Solanum tuberosum). Larsen, Knud (Department of Animal Breeding and Genetics, Danish Institute of Agricultural Sciences, Tjele, DK-8830, Den.). Journal of Plant Physiology, 162(11), 1263-1269 (English) 2005. CODEN: JPPHEY. ISSN: 0176-1617. Publisher: Elsevier GmbH.

AB A cDNA, StEN1, encoding a potato (Solanum tuberosum) **endonuclease** was cloned and sequenced. The nucleotide sequence of this clone contains an open reading frame of 906 nucleotides encoding a protein of 302 amino acids, and with a calculated mol. mass of 34.4 kDa and a Pi of 5.6. The deduced StEN1 protein contains a putative signal sequence of 25 amino acid residues. The StEN1 encoded protein shows substantial homol. to both plant and fungal **endonucleases** isolated and cloned from other sources. The highest identity (73%) was observed with AgCEL I from **celery**, Apium graveolens, ZEN1 from Zinnia elegans (69%) and DSA6 from daylily, Hemerocallis (68%). RT-PCR expression anal. demonstrated that the potato StEN1 gene is constitutively expressed in potato, although minor differences in expression level in different tissues were observed

L12 ANSWER 3 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN

2005:1256254 Efficient Genetic Mapping of Single Nucleotide Polymorphisms Based Upon DNA Mismatch Digestion. Rungis, Dainis; Hamberger, Britta; Berube, Yanik; Wilkin, Jennifer; Bohlmann, Joerg; Ritland, Kermit (Department of Forest Sciences, University of British Columbia, Vancouver, BC, V6T 1Z4, Can.). Molecular Breeding, 16(3), 261-270 (English) 2005. CODEN: MOBRFL. ISSN: 1380-3743. Publisher: Springer.

AB A single-strand specific (sss) **nuclease**, found in exts. of **celery** juice, can be used to digest heteroduplex DNA and hence identify heterozygous single nucleotide polymorphism (SNP) sites in PCR products. Here we show this method can be used to map specific genes with relative simplicity and low cost. A particular nucleotide substitution does not need to be identified, and in fact, a priori knowledge of the presence of a SNP is not required, as the entire length of the PCR product is interrogated for the presence of SNPs. This characteristic enables

application of this technique to genomes that are not well characterized with regard to SNP polymorphism, and for rapidly placing particular genes onto linkage maps. While this technique is best suited for mapping markers in a backcross configuration, we show that in an F2 configuration, where alternative homozygotes cannot be discerned by this technique, data are still relatively informative about linkage.

L12 ANSWER 4 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
2005:639882 Document No. 144:45931 A method for clone sequence confirmation
using a mismatch-specific DNA **endonuclease**. Qiu, Peter; Shandilya, Harini; Gerard, Gary F. (Transgenomic, Inc., Gaithersburg, MD, 20878, USA). Molecular Biotechnology, 29(1), 11-18 (English) 2005. CODEN: MLBOEO. ISSN: 1073-6085. Publisher: Humana Press Inc..

AB Site-directed mutagenesis and polymerase chain reaction (PCR)-based cloning are well-established methods carried out routinely in most modern mol. biol. labs. Application of these methods requires confirmation of the DNA sequence of the target gene by sequencing of DNA purified from multiple colonies, a laborious process. The authors have developed an alternative approach to screen DNA amplified directly from colony DNA for both desired and undesired mutations. This approach is based on the use of a plant mismatch DNA **endonuclease**, Surveyor **Nuclease** , to directly screen clones derived by site-directed mutagenesis. The authors have also used this approach to identify error-free clones of three genes from **celery** cDNA produced by PCR and TOPO cloning. Sequence confirmation using Surveyor **Nuclease** provides a fast and simple approach to obtain desired clones from site-directed mutagenesis and PCR-based cloning methods without the necessity of sequencing DNAs purified from multiple clones.

L12 ANSWER 5 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
2005:637377 Temperature gradient capillary electrophoresis (TGCE)-a tool for the high-throughput discovery and mapping of SNPs and IDPs. Hsia, An-Ping; Wen, Tsui-Jung; Chen, Hsin D.; Liu, Zhaowei; Yandeau-Nelson, Marna D.; Wei, Yanling; Guo, Ling; Schnable, Patrick S. (Department of Agronomy, Iowa State University, Ames, IA, 50011, USA). Theoretical and Applied Genetics, 111(2), 218-225 (English) 2005. CODEN: THAGA6. ISSN: 0040-5752. Publisher: Springer.

AB Temperature gradient capillary electrophoresis (TGCE) can be used to distinguish heteroduplex from homoduplex DNA mols. and can thus be applied to the detection of various types of DNA polymorphisms. Unlike most single nucleotide polymorphism (SNP) detection technologies, TGCE can be used even in the absence of prior knowledge of the sequences of the underlying polymorphisms. TGCE is both sensitive and reliable in detecting SNPs, small InDel (insertion/deletion) polymorphisms (IDPs) and simple sequence repeats, and using this technique it is possible to detect a single SNP in amplicons of over 800 bp and 1-bp IDPs in amplicons of approx. 500 bp. Genotyping data obtained via TGCE are consistent with data obtained via gel-based detection technologies. For genetic mapping expts., TGCE has a number of advantages over alternative heteroduplex-detection technologies such as **celery endonuclease** (CELI) and denaturing high-performance liquid chromatog. (dHPLC). Multiplexing can increase TGCE's throughput to 12 markers on 94 recombinant inbreds per day. Given its ability to efficiently and reliably detect a variety

of subtle DNA polymorphisms that occur at high frequency in genes, TGCE shows great promise for discovering polymorphisms and conducting genetic mapping and genotyping expts.

L12 ANSWER 6 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
2004:628267 Document No. 142:2913 Heteroduplex detection with a plant DNA **endonuclease** for standard gel electrophoresis. Scaffino, Manuela F.; Pilotto, Andrea; Papadimitriou, Stavros; Sbalzarini, Marco; Ansaldi, Silvia; Diegoli, Marta; Porcu, Emanuele; Grasso, Maurizia; Brega, Agnese;
Arbustini, Eloisa (Laboratorio di Diagnostica Molecolare, Area di Ricerca
Trapiantologica, IRCCS Policlinico San Matteo, Pavia, 27100, Italy). Transgenics, 4(2), 157-166 (English) 2004. CODEN: TADTEF. ISSN: 1023-6171. Publisher: Old City Publishing.
AB CEL I is a **celery**-derived **endonuclease** that cuts both strands of the heteroduplex DNA on the 3' side of any mismatch site. It has been proven to recognize heteroduplexes, both insertions/deletions and single base substitutions, in plant, human and animal genes at a rate of efficiency that varies with the sequence of the mismatch. The authors tested the sensitivity of CEL I (Transgenomic-Omaha, NE), marketed under the name SURVEYOR **Nuclease**, in 19 amplicons carrying known mutations previously identified by sequencing in 13 exons of 8 different genes (FBN1, KCNQ1, Cx26, TAZ G4.5, SCN5A, TNNT2, MYBPC3, HFE). Thirteen wild-type amplicons were used as neg. controls. The authors also tested CEL I specificity for the type of gene defects (deletions, insertions and single base substitution: purine vs. pyrimidine and vice versa). Amplicons ranging 154-400 bp in size were obtained by proofreading-Taq based PCR. The PCR conditions were maintained as in routine. Heteroduplexes were generated by a standard thermal cycler program: 95° for 10 min; 95° to 85°(-2°/s); 85° to 25°(-0.1°/s); 4°. CEL I **endonuclease** digestion was performed with 200 ng of heteroduplex DNA and controlled according to the manufacturer's SURVEYOR **Nuclease** Kit protocol. Electrophoresis was run on 2% Nusieve/1% Agarose gel. CEL I detected 17 of the 19 heteroduplexes mutations (sensitivity 90%): 3/3 deletions, 2/2 insertions and 12/14 single base substitutions. Results were confirmed in 3 sets of repeated expts. The wild-type samples did not generate any false pos. results. CEL I is a simple, fast, sensitive and reproducible tool for heteroduplexes detection.

L12 ANSWER 7 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
2004:402234 Document No. 141:18296 Mismatch cleavage by single-strand specific **nucleases**. Till, Bradley J.; Burtner, Chris; Comai, Luca; Henikoff, Steven (Basic Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA, 98109, USA). Nucleic Acids Research, 32(8),
2632-2641 (English) 2004. CODEN: NARHAD. ISSN: 0305-1048. Publisher: Oxford University Press.
AB We have investigated the ability of single-strand specific (sss) **nucleases** from different sources to cleave single base pair mismatches in heteroduplex DNA templates used for mutation and single-nucleotide polymorphism anal. The TILLING (Targeting Induced Local Lesions IN Genomes) mismatch cleavage protocol was used with the LI-COR gel detection system to assay cleavage of amplified heteroduplexes derived from a variety of induced mutations and naturally occurring

polymorphisms. We found that purified **nucleases** derived from **celery** (CEL I), mung bean sprouts and Aspergillus (S1) were able to specifically cleave nearly all single base pair mismatches tested. Optimal nicking of heteroduplexes for mismatch detection was achieved using higher pH, temperature and divalent cation conditions than are routinely used for digestion of single-stranded DNA. Surprisingly, crude plant exts. performed as well as the highly purified prepns. for this application. These observations suggest that diverse members of the S1 family of sss **nucleases** act similarly in cleaving non-specifically at bulges in heteroduplexes, and single-base mismatches are the least accessible because they present the smallest single-stranded region for enzyme binding. We conclude that a variety of sss **nucleases** and exts. can be effectively used for high-throughput mutation and polymorphism discovery.

L12 ANSWER 8 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
2004:312039 Document No. 140:418712 Mutation detection using Surveyor **nuclease.** Qiu, Peter; Shandilya, Harini; D'Alessio, James M.; O'Connor, Kevin; Durocher, Jeffrey; Gerard, Gary F. (Transgenomic, Gaithersburg, MD, 20878, USA). BioTechniques, 36(4), 702-704,706-707 (English) 2004. CODEN: BTNQDO. ISSN: 0736-6205. Publisher: Eaton Publishing Co..

AB A simple and flexible mutation detection technol. was developed for the discovery and mapping of both known and unknown mutations. This technol. is based on a new mismatch-specific DNA **endonuclease** from **celery**, Surveyor **nuclease**, which is a member of the CEL **nuclease** family of plant DNA **endonucleases.** Surveyor **nuclease** cleaves with high specificity at the 3' side of any mismatch site in both DNA strands, including all base substitutions and insertion/deletions up to at least 12 nucleotides. Surveyor **nuclease** technol. involves four steps: (i) PCR to amplify target DNA from both mutant and wild-type reference DNA; (ii) hybridization to form heteroduplexes between mutant and wild-type reference DNA; (iii) treatment of annealed DNA with Surveyor **nuclease** to cleave heteroduplexes; and (iv) anal. of digested DNA products using the detection/separation platform of choice. The technol. is highly sensitive, detecting rare mutants present at as low as 1 in 32 copies. Unlabeled Surveyor **nuclease** digestion products can be analyzed using conventional gel electrophoresis or high-performance liquid chromatog. (HPLC), while end-labeled digestion products are suitable for anal. by automated gel or capillary electrophoresis. The entire protocol can be performed in less than a day and is suitable for automated and high-throughput procedures.

L12 ANSWER 9 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
2002:778172 Document No. 137:289893 Enzymic substitution of base mismatches in heteroduplexes in the generation of sequence diversity in DNA shuffling. Padgett, Hal S.; Fitzmaurice, Wayne P.; Lindo, John A. (Large Scale Biology Corporation, USA). PCT Int. Appl. WO 2002079468 A2 20021010, 105 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,

OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW. (English). CODEN: PIXXD2. APPLICATION: WO 2002-US3055 20020201. PRIORITY: US 2001-2001/PV26638U 20010202; US 2001-2001/PV268785 20010214.

AB We describe here an in vitro method of increasing complementarity in a heteroduplex polynucleotide sequence in an analog of base mismatch repair. The method uses annealing of opposite strands to form a polynucleotide duplex with mismatches. The heteroduplex polynucleotide is combined with an effective amount of enzymes having strand cleavage activity, 3' to 5' exonuclease activity, and polymerase activity, and allowing sufficient time for the percentage of complementarity to be increased within the heteroduplex. Not all heteroduplex polynucleotide will necessarily have all mismatches resolved to complementary. The resulting polynucleotide is optionally ligated. Several variant polynucleotides result. At sites where either of the opposite strands has templated recoding in the other strand, the resulting percent complementarity of the heteroduplex polynucleotide sequence is increased. The parent polynucleotides need not be cleaved into fragments prior to annealing heterologous strands. Therefore, no reassembly is required and the removal of base mismatch may help to lower the level of artifacts associated with PCR amplification of the shuffling products. Optimization of conditions for use of the CEL-I repair **nuclease** of **celery** to cleave at base mismatches are described. The utility of the method is shown by using it to restore restriction cleavage sites that had been lost by cleavage and ligation. The method was used to create variants of green fluorescent protein during optimization expts. Use of the method with widely divergent genes for movement proteins of tobamoviruses is demonstrated.

L12 ANSWER 10 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN

2001:636264 Document No. 135:206492 Polynucleotides encoding mismatch **endonuclease** CELI and diagnostic and therapeutic uses thereof. Yeung, Anthony T. (Fox Chase Cancer Center, USA). PCT Int. Appl. WO 2001062974 A1 20010830, 93 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT,

AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2001-US5502 20010222. PRIORITY: US 2000-510322 20000222; US 2000-514768 20000228.

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6699980

AB The invention claims polynucleotide and polypeptide sequences for a mismatch **endonuclease** named CEL I and a purified, active 39 kD protein which is a putative CEL II isoenzyme. Use of CEL I polynucleotide sequences in recombinant production of an **endonuclease**, genetic vectors, and host cells are claimed. In addition, methods for screening compds. which modulate CEL I **endonuclease** activity and antibodies specific for an **endonuclease** are claimed. The invention further claims methods for use of CEL I **endonuclease** for the detection of mutations in targeted polynucleotide sequences, to facilitate the localization and identification of mutations, mismatches and genetic polymorphisms. Methods for detecting mutations using CEL I **endonuclease** involve exposing hybridized, labeled polynucleotides to the enzyme and

identifying the cleaved enzyme products in the cases where mismatched sequences were present. Amino acid sequences encoding Arabidopsis thaliana BFN1 (bifunctional **nuclease** 1), Zinnia elegans **endonuclease** ZEN1, and Hemerocallis DSA6 (daylily senescence-associated protein 6) are greater than 60% identical to CEL I **endonuclease** and use of these polypeptides by the methods of this invention is claimed. Mutations in the BRCA1 gene were analyzed using CEL I **endonuclease** and Genescan fragment anal. on an automated DNA sequencer. BRCA1 DNA was amplified using PCR and one strand was labeled with 5'-FAM, the other with TET. Two-color heterduplexes were incubated with CEL I mismatch **endonuclease** and mismatch-specific cleavage was observed

L12 ANSWER 11 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
2000:477621 Document No. 133:330104 CEL I enzymatic mutation detection assay. Kulinski, J.; Besack, D.; Oleykowski, C. A.; Godwin, A. K.; Yeung, A. T. (Fox Chase Cancer Center, Philadelphia, PA, 19111, USA). BioTechniques, 29(1), 44, 46, 48 (English) 2000. CODEN: BTNQDO. ISSN: 0736-6205. Publisher: Eaton Publishing Co..

AB This method is simple and dependable. CEL I is an **endonuclease** isolated from **celery**, and is the first known **endonuclease** to have high specificity for insertions, deletion and base-substitution mismatches. The assay uses fluorescently or radioactively labeled nucleotides for fragment detection. Briefly, PCR is used to amplify the normal and mutant alleles of the target sequence. The authors present the optimized conditions for the CEL I mutation detection assay.

L12 ANSWER 12 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
2000:435789 Document No. 133:190327 In vitro host range studies with a new baculovirus isolate from the diamondback moth Plutella xylostella (L.) (Plutellidae: Lepidoptera). Kariuki, C. W.; Mcintosh, A. H.; Goodman, C. L. (Department of Entomology, University of Missouri, Columbia, MO, 65211, USA). In Vitro Cellular & Developmental Biology: Animal, 36(4), 271-276 (English) 2000. CODEN: IVCAED. ISSN: 1071-2690. Publisher: Society for In Vitro Biology.

AB The in vitro host range of a newly isolated baculovirus from the diamondback moth Plutella xylostella was tested against six lepidopteran cell lines. Two baculoviruses with wide host ranges from the alfalfa looper Autographa californica (A. californica multiple nucleopolyhedrovirus, AcMNPV) and the **celery** looper Anagrapha falcifera (AfMNPV) were also included in this study for comparative purposes. PxMNPV replicated in all six cell lines and produced occlusion bodies, with HV-AM1 and TN-CL1 cells producing the highest viral titers and greatest number of occlusion bodies. There was no significant replication of AcMNPV and AfMNPV in the HZ-FB33 cell line and thus no production of occlusion bodies. The restriction **endonuclease** profiles of the three baculoviruses showed similarities but could be readily distinguished from each other. Either HV-AM1 or TN-CL1 would be suitable cell lines for the in vitro production of PxMNPV.

L12 ANSWER 13 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN

2000:152319 Document No. 132:331182 Purification, Cloning, and Characterization of the CEL I **Nuclease.** Yang, Bing; Wen, Xiao; Kodali, Nagendra S.; Oleykowski, Catherine A.; Miller, C. Glenn; Kulinski, Joanne; Besack, David; Yeung, Jason A.; Kowalski, David; Yeung, Anthony T. (Fox Chase Cancer Center, Philadelphia, PA, 19111, USA). Biochemistry, 39(13), 3533-3541 (English) 2000. CODEN: BICHAW. ISSN: 0006-2960. Publisher: American Chemical Society.

AB CEL I, isolated from **celery**, is the first eukaryotic **nuclease** known that cleaves DNA with high specificity at sites of base-substitution mismatch and DNA distortion. The enzyme requires Mg2+ and Zn2+ for activity, with a pH optimum at neutral pH. We have purified CEL I 33 000-fold to apparent homogeneity. A key improvement is the use of α-methyl-mannoside in the purification buffers to overcome the aggregation of glycoproteins with endogenous lectins. The SDS gel electrophoresis band for the homogeneous CEL I, with and without the removal of its carbohydrate moieties, was extracted, renatured, and shown to have mismatch cutting specificity. After determination of the amino acid sequence of 28% of the CEL I polypeptide, we cloned the CEL I cDNA. Potential orthologs are **nucleases** putatively encoded by the genes BFN1 of Arabidopsis, ZEN1 of Zinnia, and DSA6 of daylily. Homologies of CEL I with S1 and P1 **nucleases** are much lower. We propose that CEL I exemplifies a new family of neutral pH optimum, magnesium-stimulated, mismatch duplex-recognizing **nucleases**, within the S1 superfamily.

L12 ANSWER 14 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN

1999:54744 Document No. 130:219755 Incision at Nucleotide Insertions/Deletions and Base Pair Mismatches by the SP **Nuclease** of Spinach. Oleykowski, Catherine A.; Mullins, Colleen R. Bronson; Chang, David W.; Yeung, Anthony T. (Fox Chase Cancer Center, Philadelphia, PA, 19111, USA). Biochemistry, 38(7), 2200-2205 (English) 1999. CODEN: BICHAW. ISSN: 0006-2960. Publisher: American Chemical Society.

AB Spinach leaves contain a highly active **nuclease** called SP. The purified enzyme incises single-stranded DNA, RNA, and double-stranded DNA that has been destabilized by A-T-rich regions and DNA lesions. This broad range of activity has suggested that SP may be similar to a family of **nucleases** represented by S1, P1, and the mung bean **nuclease.** However, unlike these single-stranded **nucleases** that require acidic pH and low ionic strength conditions, SP has a neutral pH optimum and is active over a wide range of salt concns. We have extended these findings and showed that an outstanding substrate for SP is a mismatched DNA duplex. For base-substitution mismatches, SP incises at all mismatches except those containing a guanine residue. SP also cuts at insertion/deletions of one or more nucleotides. Where the extrahelical DNA loop contains one nucleotide, the preference of extrahelical nucleotide is A » T .apprx. C but undetectable at G. The inability of SP to cut at guanine residues and the favoring of A-T-rich regions distinguish SP from the CEL I family of neutral pH mismatch **endonucleases** recently discovered in **celery** and other plants. SP, like CEL I, does not turn over after incision at a mismatched site in vitro. Similar to CEL I, the presence of a DNA polymerase or a DNA ligase allows SP to turn over and stimulate its activity in vitro by about 20-fold. The possibility that the SP **nuclease** may be a natural variant of the CEL I family of mismatch **endonucleases** is discussed.

L12 ANSWER 15 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
1998:727718 Document No. 130:76748 Mutation detection using a novel plant **endonuclease.** Oleykowski, Catherine A.; Mullins, Colleen R. Bronson; Godwin, Andrew K.; Yeung, Anthony T. (Fox Chase Cancer Center, Philadelphia, PA, 19111, USA). Nucleic Acids Research, 26(20), 4597-4602
(English) 1998. CODEN: NARHAD. ISSN: 0305-1048. Publisher: Oxford University Press.

AB We have discovered a useful new reagent for mutation detection, a novel **nuclease** CEL I from **celery.** It is specific for DNA distortions and mismatches from pH 6 to 9. Incision is on the 3'-side of the mismatch site in one of the two DNA strands in a heteroduplex. CEL I-like **nucleases** are found in many plants. We report here that a simple method of enzyme mutation detection using CEL I can efficiently identify mutations and polymorphisms. To illustrate the efficacy of this approach, the exons of the BRCA1 gene were amplified by PCR using primers 5'-labeled with fluorescent dyes of two colors. The PCR products were annealed to form heteroduplexes and subjected to CEL I incision. In GeneScan analyses with a PE Applied Biosystems automated DNA sequencer, two independent incision events, one in each strand, produce truncated fragments of two colors that complement each other to confirm the position of the mismatch. CEL I can detect 100% of the sequence variants present, including deletions, insertions and missense alterations. Our results indicate that CEL I mutation detection is a highly sensitive method for detecting both polymorphisms and disease-causing mutations in DNA fragments as long as 1120 bp in length.

L12 ANSWER 16 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
1998:1594 Document No. 128:72368 Mismatch **endonuclease** CEL I from **celery** and uses thereof in identifying mutations in targeted polynucleotide strands. Yeung, Anthony T. (Fox Chase Cancer Center, USA).

PCT Int. Appl. WO 9746701 A1 19971211, 81 pp. DESIGNATED STATES: W: AU, CA, JP, MX; RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1997-US8705 19970520. PRIORITY: US 1996-658322 19960605; US 1997-803621 19970221.

AB An **endonuclease** isolated from **celery**, CELI, is disclosed as well as methods for use in detection of mutations in targeted polynucleotides. The methods facilitate localization and identification of mutations, mismatches and polymorphisms. The enzyme recognizes every type of mismatch regardless of the sequence context in which the mismatch resides and the enzyme is active in pH ranges from acidic to basic. To detect the presence of a mutation in a target DNA sequence, the target is converted into single stranded DNA and hybridized with a non-mutated DNA. The sequences are then amplified by PCR, labeled with a detectable marker, hybridized to one another, and exposed to **endonuclease** CELI of the present patent, and analyzed on gels for the presence of the mutation. The mismatched mutation site is cleaved by the CELI **endonuclease** resulting in characteristic DNA fragments in the gel electrophoresis.

L12 ANSWER 17 OF 17 CAPLUS COPYRIGHT 2006 ACS on STN
1990:418947 Document No. 113:18947 Production of male-sterile plants and

seeds by recombinant DNA methods. Mariani, Celestina; Leemans, Jan; De Greef, Willy; De Beuckeleer, Marc (Plant Genetic Systems N. V., Belg.). PCT Int. Appl. WO 8910396 A1 19891102, 86 pp. DESIGNATED STATES: W: AU, DK, FI, HU, JP, US. (English). CODEN: PIXXD2. APPLICATION: WO 1989-EP495 19890427. PRIORITY: GB 1988-10120 19880428.

AB Male-sterile plants and seed are produced from plant cells transformed with a gene that disturbs the metabolism, function, or development of the stamen. The 5' flanking region of the Nicotiana tabacum anther-specific gene TA29gene was cloned and fused to gene 4 of Agrobacterium T-DNA. Gene 4 encodes isopentenyl transferase, the overexpression of which causes enhanced production of cytokinin, which disturbs metabolism and organogenesis of the tapetum cells.). The plasmid containing this construct was used to prepare transgenic tobacco plants by standard techniques. No functional tapetum cells were found in the anthers of the flowers of these transgenic tobacco plants.

```
=> S L7 AND L5
L13          29 L7 AND L5

=> S L8 AND L5
L14           2 L8 AND L5

=> S (L13,L14) NOT L13
L15           0 ((L13 OR L14)) NOT L13

=> S PURIFICA?
         318868 PURIFICA?
         288407 PURIFN
            236 PURIFNS
         288510 PURIFN
                  (PURIFN OR PURIFNS)
L16      469713 PURIFICA?
                  (PURIFICA? OR PURIFN)

=> S SEPARAT?
         342883 SEPARAT?
         277672 SEP
          12597 SEPS
         289072 SEP
                  (SEP OR SEPS)
         449939 SEPD
              1 SEPDS
         449940 SEPD
                  (SEPD OR SEPDS)
          93884 SEPG
              1 SEPGS
          93885 SEPG
                  (SEPG OR SEPGS)
         561871 SEPN
          36412 SEPNS
         580296 SEPN
                  (SEPN OR SEPNS)
L17     1382528 SEPARAT?
                  (SEPARAT? OR SEP OR SEPD OR SEPG OR SEPN)

=> S (L16,L17) AND (L7,L8)
```

L18 9 ((L16 OR L17)) AND ((L7 OR L8))

=> S L18 NOT L13
L19 6 L18 NOT L13

=> D 1-6 CBIB ABS

L19 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN
2004:320598 Document No. 141:49301 Characterization of recombinant **CEL-I**, a GalNAc-specific C-type lectin, expressed in Escherichia coli using an artificial synthetic gene. Hatakeyama, Tomomitsu; Shiba, Kouhei; Matsuo, Noriaki; Fujimoto, Tokiko; Oda, Tatsuya; Sugawara, Hajime; Aoyagi, Haruhiko (Department of Applied Chemistry, Faculty of Engineering, Nagasaki University, Nagasaki, 852-8521, Japan). Journal of Biochemistry (Tokyo, Japan), 135(1), 101-107 (English) 2004. CODEN: JOBIAO. ISSN: 0021-924X. Publisher: Japanese Biochemical Society.

AB **CEL-I** is a C-type lectin isolated from the Holothuroidea Cucumaria echinata. This lectin shows very high N-acetylgalactosamine-binding specificity. We constructed an artificial gene encoding recombinant **CEL-I** (rCEL-I) using a combination of synthetic oligonucleotides, and expressed it in Escherichia coli cells. Since the recombinant protein was obtained as inclusion bodies, the latter were solubilized using urea and 2-mercaptoethanol, and the protein was refolded during the **purification** and dialysis steps. The purified rCEL-I showed comparable hemagglutinating activity to that of native **CEL-I** at relatively high Ca2+-concns., whereas it was weaker at lower Ca2+-concns. due to decreased Ca2+-binding affinity. RCEL-I exhibited similar carbohydrate-binding specificity to native **CEL-I**, including strong GalNAc-binding specificity, as examined by hemagglutination inhibition assay. Comparison of the far UV-CD spectra of recombinant and native **CEL-I** revealed that the two proteins undergo a similar conformational change upon binding of Ca2+. Single crystals of rCEL-I were also obtained under the same conditions as those used for the native protein, suggesting that they have similar tertiary structures. Although native **CEL- I** exhibited strong cytotoxicity toward cultured cells, rCEL-I showed low cytotoxicity. These results indicate that rCEL-I has a tertiary structure and carbohydrate-binding specificity similar to those of native **CEL-I**. However, there is a subtle difference in the properties between the two proteins probably due to the addnl. methionine residue at the N-terminus of rCEL-I.

L19 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN
2000:152319 Document No. 132:331182 **Purification**, Cloning, and Characterization of the **CEL I** Nuclease. Yang, Bing; Wen, Xiao; Kodali, Nagendra S.; Oleykowski, Catherine A.; Miller, C. Glenn; Kulinski, Joanne; Besack, David; Yeung, Jason A.; Kowalski, David; Yeung, Anthony T. (Fox Chase Cancer Center, Philadelphia, PA, 19111, USA). Biochemistry, 39(13), 3533-3541 (English) 2000. CODEN: BICHAW. ISSN: 0006-2960. Publisher: American Chemical Society.

AB **CEL I**, isolated from celery, is the first eukaryotic nuclease known that cleaves DNA with high specificity at sites of base-substitution mismatch and DNA distortion. The enzyme requires Mg2+ and Zn2+ for activity,

with a pH optimum at neutral pH. We have purified **CEL I** 33 000-fold to apparent homogeneity. A key improvement is the use of α-methyl-mannoside in the **purifn** . buffers to overcome the aggregation of glycoproteins with endogenous lectins. The SDS gel electrophoresis band for the homogeneous **CEL I**, with and without the removal of its carbohydrate moieties, was extracted, renatured, and shown to have mismatch cutting specificity. After determination of the amino acid sequence of 28% of the **CEL I** polypeptide, we cloned the **CEL I** cDNA. Potential orthologs are nucleases putatively encoded by the genes BFN1 of Arabidopsis, ZEN1 of Zinnia, and DSA6 of daylily. Homologies of **CEL I** with S1 and P1 nucleases are much lower. We propose that **CEL I** exemplifies a new family of neutral pH optimum, magnesium-stimulated, mismatch duplex-recognizing nucleases, within the S1 superfamily.

L19 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN
1994:598882 Document No. 121:198882 **Purification** and characterization of four Ca2+-dependent lectins from the marine invertebrate, Cucumaria echinata. Hatekeyama, Tomomitsu; Kohzaki, Hidetsugu; Nagatomo, Haruna; Yamasaki, Nobuyuki (Fac. Agric., Kyushu Univ., Fukuoka, 812, Japan). Journal of Biochemistry (Tokyo, Japan), 116(1), 209-14 (English) 1994. CODEN: JOBIAO. ISSN: 0021-924X.
AB Four Ca2+-dependent, N-acetylgalactosamine/galactose-specific lectins were purified from the marine invertebrate, Cucumaria echinata (Holothuroidea), by column chromatog. on lactosyl-Sepharose 4B, Sephacryl S-200, and Q-Sepharose. The mol. masses of these lectins were estimated to be 27 kDa (**CEL-I**), 35 kDa (**CEL-II**), 45 kDa (CEL-III), and 68 kDa (CEL-IV) on SDS-PAGE under nonreducing conditions. Among these lectins, **CEL-I** and CEL-IV strongly agglutinated rabbit and human erythrocytes, and were found to recognize N-acetylgalactosamine and galactose-containing carbohydrates from the results of a hemagglutination inhibition assay. In contrast, **CEL- II** failed to agglutinate any erythrocytes tested, although its carbohydrate-binding ability was confirmed by a carbohydrate-binding assay involving asialofetuin-horseradish peroxidase. Interestingly, CEL-III caused hemolysis of rabbit and human erythrocytes, while it showed only hemagglutination of chicken and horse erythrocytes at relatively high concns. The hemolytic activity of CELL-III was also dependent on the Ca2+-concentration, and inhibited by N-acetylgalactosamine and galactose-containing carbohydrates, suggesting that the hemolysis was caused by Ca2+-dependent binding of CEL-III to specific carbohydrate chains on the erythrocyte surface and the following partial destruction of the membrane.

L19 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN
1966:36080 Document No. 64:36080 Original Reference No. 64:6708a-h,6709a-b Alkaloids of Melodinus australis. Linde, Horst H. A. (Univ. Basel, Switz.). Helvetica Chimica Acta, 48(8), 1822-42 (German) 1965. CODEN: HCACAV. ISSN: 0018-019X.
GI For diagram(s), see printed CA Issue.
AB Powdered bark (38.5 kg.) of M. australis was extracted with 656 kg. MeOH in 10 portions and each portion was concentrated to give a total of 12.356 kg. concentrates. The combined concentrates 1 and 10 (6.16 kg.) were diluted with 1 l. MeOH, acidified with 320 ml. AcOH in 13 l. H2O, kept 48 hrs. at -5°, and the yellow brown precipitate (I) was filtered over Hyflo Super **Cel** (**II**) and washed with 8 ml. AcOH in 350 ml. H2O and

50 ml. MeOH. The concentrated filtrate (5 l.) was extracted 3 times with 3 l. Et2O and the washed (2% AcOH) and dried extract evaporated, giving a residue (III). The aqueous acid solution was adjusted with NH4OH to pH 9-10, extracted 8 times with 3 l. Et2O (filtering each time the emulsions formed through II, and extracting the filter cake with Et2O) and the washed (30% NaCl) extract evaporated to give 89.5 g. residue (IV). The aqueous solution was mixed with 150 ml. 50% KOH, extracted with CHCl3, and the washed (H2O) and dried extract evaporated in vacuo to give 12.1 g. residue (V). The MeOH exts. 2-9 were worked up in the same way, giving, together with 28.16 g. III, 26.8 g. residue from the Et2O extract of the NH4OH neutralized solution, and 3.56 g. (VI) from the CHCl3 extract of the alkaline solution The combined I were stirred 2 hrs. in a mixture of 160 ml. AcOH, 6.5 l. H2O, and 250 ml. MeOH and the filtrate was worked up as above to give 7.53 g. residue from AcOH-acid solution, 37.78 g. from the NH4OH-neutral solution, and 10.39 g. from the CHCl3 extract of the alkaline solution The total yield of crude alkaloids (VII) was 180.13 g. or 0.47%. All products were worked up by chromatography: e.g. 20 g. IV, chromatographed over 600 g. Al2O3 gave 42 fractions. Fraction 2, eluted with petroleum ether (P.E.)-C6H6 (1:1) gave 33 mg. (all yields based on VII) (--)-quebrachamine, prisms, m. 143-5° (Et2O-P.E.), [α]19D -106° (c 0.997, all in CHCl3). Rechromatography of fractions 3-7 [6.895 g., eluted with P.E.-C6H6 (1:1)] gave 6.5 g. venalstonine (VIIa), m. 138-42° (Et2O-P.E.), [α]23D -88.8° (c 1.406); 260 mg. venalstonidine (VIII), m. 230-6° (CHCl3-Et2O), [α]22D -95.5° (c 1.43); 3.3 g. condylocarpine, m. 163-9° (Et2O), [α]22D 889° (c 0.426); and 425 mg. (+)-17-methoxyquebrachamine (IX), m. 157-60°, [α]22D 68° → 115° (c 1.3). Rechromatography of fractions 8-12 [790 mg., eluted with P.E.-C6H6 (1:3) and C6H6] gave 70 mg. of a dimeric alkaloid, C41H46O3N4, sintering at 220° followed by carbonization. [α]23D 54° (c 0.830). Rechromatography of fractions 13-15 [380 mg., eluted with C6H6 and C6H6-CHCl3 (19:1)] gave traces of an alkaloid, prisms, m. 186-95° (Et2OC5H12), [α]24D 112.2° (c 0.401), and 105 mg. alkaloid, C20H24O2N2, prisms, m. 170-5° (Et2O), [α]23D 177° (c 1.075). Rechromatography of fractions 16-19 [405 mg., eluted with C6H6-CHCl3 (19:1 and 9:1)], 25-30 [1.590 g., eluted with C6H6-CHCl3 (3:2 and 3:7)], and 36-42 [2.965 g., eluted with CHCl3-MeOH (99:1, 95:5, and 9:1)] gave no crystalline products. Rechromatography of fractions 20-24 (1.833 g., eluted with C6H6-CHCl3 (9:1 and 4:1)] gave 415 mg. alkaloid, C19H22ON2, m. 214-16° (CHCl3-Et2O), [α]24D -421° (c 0.973). Fractions 31-35 [1.68 g., eluted with C6H6-CHCl3 (3:7) and CHCl3] gave 104 mg. stemmadenine, m. 189-93° (MeOH-CHCl3-Et2O), [α]19D 313° (c 0.527, C5H5N); and 192 mg. akuammidine, m. 238-43°, [α]21D 14.6° (c 1.17, C5H5N). The non-polar fractions of the chromatographs were extracted in CHCl3 with 2N HCl, the acid exts. made alkaline with NH4OH and extracted with Et2O to give 5.2 g. bases (X); the washed and dried CHCl3 phase was evaporated to give 3.4 g. neutral products (XI). Chromatography of X over Al2O3 gave 9 mg. alkaloid (XII), C21H22O4N2, m. 245-8° (CHCl3-Et2O), [α]24D -48.4° (c 0.223), -55.1° (c 0.49); and 35 mg. alkaloid (XIII), C21H22O3N2, prisms, m. 227-31° (CHCl3-Et2O), [α]20D -99° (c 0.699). Chromatography of the combined fractions V and VI gave 6.15 mg. alkaloid (XIV), C21H26O3N2, m. 190-7°, (CHCl3-Et2O), [α]23D -62° (c 1.142), and 250 mg. alkaloid, C21H26O3N2 (XV), m. 187-92° (CHCl3-Et2O), [α]23D -63° (c 1.037). The neutral fractions III and VI (7.55 g.) were treated with CH2N2 in Et2O and separated into 14% basic, 11% acid, and

44.5% neutral fractions; chromatography of the last gave no crystalline product. Hydrogenation of 157 mg. VIIa in 20 ml. EtOH with Pd-C gave 105 mg. copsinine, m. 100-3° (Et2O-P.E.), [α]21D -70.5° (c 1.961). Hydrogenation of 32 mg. XIII (m. 225-8°) in EtOH 4 hrs. at 20° gave 16 mg. copsinine-6-ring-lactam (dihydro-XIII) (XVI), m. 207-9° (CHCl3-Et2O), [α]25D -18.3° (c 1.07). Hydrogenation of 7 mg. XII followed by thin layer chromatography and spraying with Ce(SO4)2-H2SO4 showed the presence of 3 products, none of which had the Rf value of XIII and XVI. Uv spectral data were given for the compds.

L19 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN

1963:447940 Document No. 59:47940 Original Reference No. 59:8606h,8607a-d Prostoglondins and related factors. XVI. Structure and synthesis of a derivative of prostaglandin E1. Samuelsson, Bengt; Stallberg, Gunnèl (Karolinska Inst., Stockholm). Acta Chemica Scandinavica, 17(3), 810-16 (English) 1963. CODEN: ACHSE7. ISSN: 0904-213X.

GI For diagram(s), see printed CA Issue.

AB cf. CA 57, 10192g; 58, 4884b; 59, 5031d. Prostaglandin E1 (I) was reduced catalytically in acidic medium. The least polar compound in the reaction mixture was **separated** by reversed phase partition chromatography on hydrophobic Super-**Cel**(**II**). This compound treated with alkali gave 2-(6-carboxyhexyl)-3-octylcyclopent-2-enone (III). III was prepared by cyclization of Me 9,12-dioxo-10-carbomethoxyeicosanoate (IV) and by cyclization of 4-octyl-4-(7-carbomethoxyheptyl)-γ-butyrolactone (V). Nonanoyl bromide (13.7 g.) treated with CH2N2 in ether at 0° and then with HBr gave 12.8 g. 1-bromodecan-2-one (VI), b0.2 91°, m. 26.7-7.5°, n25D 1.4640. VI (11.4 g.) was added to the Na derivative of di-Me 3-oxoundecane-1,11-dicarboxylate (VII) (prepared by overnight-refluxing with granulated Na in ether), the mixture heated 3 hrs. at 50°, acidified with dilute H2SO4, and extracted with ether. The ether extract was washed, dried, and concentrated to give 19.6 g. crude IV, which was dissolved in a solution of 15 g. NaOH in 450 ml. 50% alc., heated 3 hrs. at 65°, the alc. partly distilled, the solution heated 0.5 hr. at 100° with dilute H2SO4, and the product extracted with ether to give a mixture of III and 2-heptyl-3-(7-carbomethoxyheptyl)cyclopent-2-enone (VIII). III, λ 237 mμ (ε 14,200), and VIII, λ 237 mμ (ε 12,100), were **separated** by chromatography on II. The Na derivative of VII (prepared from 4.9 g. VII and NaOEt) was treated with 2 ml. ClCH2CO2Et, the mixture refluxed 5 hrs., filtered, and the filtrate evaporated in vacuo. The residue was refluxed 7 hrs. with 10 ml. concentrated HCl, the reaction mixture evaporated in vacuo, the residue dissolved in 20 ml. MeOH saturated with HCl, and kept 20 hrs. at room temperature The solvent was evaporated, the residue dissolved in ether, washed with 5% Na2CO3 and water, dried, and evaporated to give 4.1 g. di-Me 4-oxododecane-1,12- dicarboxylate (IX), oil. A Grignard reaction with IX and C8H17MgBr gave crude V, which was treated with polyphosphoric acid and the product refluxed 2 hrs. in N NaOH in 80% MeOH to give III and VIII. The results support the proposed structure of I (CA 57, 11037i) and prove its carbon skeleton.

L19 ANSWER 6 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN

1961:24785 Document No. 55:24785 Original Reference No. 55:4892d-g Amine salts of penicillin. Culik, Karel; Toscani, Vladimir; Vondracek, Miloslav

CS 88685 19590215 (Unavailable). APPLICATION: CS .

AB A method is described based on the precipitation of a slightly soluble salt of penicillin in the presence of an adsorption medium, such as active C, earth, cellulose, Al2O3, or diatomaceous earth (Hyflo-Super Cel). The following examples are given: (1) The 1st concentrate from the production of penicillin (220 l., potency 31,700 I.U./ml., i.e. 6.96 + 109 I.U. containing 6.62 + 109 I.U. of penicillin G) was cooled to 2° and the pH was adjusted to 1.9 with 50% H3PO4 and extracted with 130 l. BuOAc. The organic phase was dried with Na2SO4, suspended with 1.5 kg. Super Cel, and neutralized with stirring with 50% N-ethylpiperidine in BuOAc to pH 8.0-8.5. The mixture was kept for 2 hrs. at 0-3°, filtered, and the contaminants were removed with Me2CO to give 6290 g. mixture of the N-ethylpiperidine salt of penicillin (I) with Super Cel, i.e. 4790 g. I of potency 1010 I.U./mg. corresponding to 91% of the total activity and 95.5% of activity of penicillin G. I was worked up as follows: I (3145 g.) was suspended in 15 l. CHCl3, and the solution was separated from Super Cel, decolorized by filtration with 50 g. active C, and precipitated with 5% solution of AcOK in BuOH to give 1878 g. K salt of penicillin of the potency 1570 I.U./mg., i.e. 2.97 + 109 I.U. Similarly, 3145 g. I was suspended in 18 l. H2O. The Super Cel was filtered, the solution was decolorized with active C, and treated in the cold with a solution of 1600 g. procaine-HCl in 2800 ml. H2O to give 3011 g. procaine penicillin of the potency 3560 I.U./mg., i.e. 3.04 + 109 I.U.

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=> E GERARD G/AU
=> S E3,E4,E7-E9
             33 "GERARD G"/AU
              1 "GERARD G F"/AU
              6 "GERARD GARY"/AU
             53 "GERARD GARY F"/AU
              2 "GERARD GARY FLOYD"/AU
L20          95 ("GERARD G"/AU OR "GERARD G F"/AU OR "GERARD GARY"/AU OR
"GERARD
                GARY F"/AU OR "GERARD GARY FLOYD"/AU)

=> E SHANDILYA/AU
=> S E5-E7
             10 "SHANDILYA HARINI"/AU
              5 "SHANDILYA HARISH"/AU
              3 "SHANDILYA HARISH K"/AU
L21          18 ("SHANDILYA HARINI"/AU OR "SHANDILYA HARISH"/AU OR "SHANDILYA
                HARISH K"/AU)

=> E QIU P/AU
=> S E3,E35
             19 "QIU P"/AU
              3 "QIU PETER"/AU
L22          22 ("QIU P"/AU OR "QIU PETER"/AU)

=> E D ALESSIO J/AU
=> S E3,E4,E6-E8
              3 "D ALESSIO J"/AU
              2 "D ALESSIO J M"/AU
              2 "D ALESSIO JAMES"/AU
             16 "D ALESSIO JAMES M"/AU
              1 "D ALESSIO JAMES MICHAEL"/AU
```

L23 24 ("D ALESSIO J"/AU OR "D ALESSIO J M"/AU OR "D ALESSIO JAMES"/AU
OR "D ALESSIO JAMES M"/AU OR "D ALESSIO JAMES MICHAEL"/AU)

=> S L20,L21,L22,L23
L24 141 (L20 OR L21 OR L22 OR L23)

=> S L24 AND (L7,L9)
L25 4 L24 AND ((L7 OR L9))

=> S L25 NOT (L13,L19)
L26 3 L25 NOT ((L13 OR L19))

=> D 1-3 CBIB ABS

L26 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2006 ACS on STN
2006:54886 Document No. 144:145421 Cloning, purification and sequence of DNA
mismatch-specific endonuclease CELII from **celery**.
Shandilya, Harini; Gerard, Gary F.; Qui, Peter
(Transgenomic, Inc., USA). PCT Int. Appl. WO 2006007124 A2 20060119, 59 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IS, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2005-US17508 20050518. PRIORITY: US 2004-2004/PV580450 20040617.

AB The present invention relates to isolated cDNA sequences encoding CELII DNA mismatch-specific endonuclease from **celery** and vectors and host cells for producing a protein encoded thereby. A modified purification method was developed that separated CELI and CELII endonucleases. The cDNA sequence and the encoded amino acid sequence of CELII from **celery** are disclosed.

L26 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2006 ACS on STN
2005:639882 Document No. 144:45931 A method for clone sequence confirmation
using a mismatch-specific DNA endonuclease. **Qiu, Peter; Shandilya, Harini; Gerard, Gary F.** (Transgenomic, Inc., Gaithersburg, MD, 20878, USA). Molecular Biotechnology, 29(1), 11-18 (English) 2005. CODEN: MLBOEO. ISSN: 1073-6085. Publisher: Humana Press
Inc..

AB Site-directed mutagenesis and polymerase chain reaction (PCR)-based cloning are well-established methods carried out routinely in most modern mol. biol. labs. Application of these methods requires confirmation of the DNA sequence of the target gene by sequencing of DNA purified from multiple colonies, a laborious process. The authors have developed an alternative approach to screen DNA amplified directly from colony DNA for both desired and undesired mutations. This approach is based on the use of a plant mismatch DNA endonuclease, Surveyor Nuclease, to directly screen clones derived by site-directed

mutagenesis. The authors have also used this approach to identify error-free clones of three genes from **celery** cDNA produced by PCR and TOPO cloning. Sequence confirmation using Surveyor Nuclease provides a fast and simple approach to obtain desired clones from site-directed mutagenesis and PCR-based cloning methods without the necessity of sequencing DNAs purified from multiple clones.

L26 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2006 ACS on STN
2004:312039 Document No. 140:418712 Mutation detection using Surveyor nuclease. **Qiu, Peter; Shandilya, Harini; D'Alessio, James M.**; O'Connor, Kevin; Durocher, Jeffrey; **Gerard, Gary F.** (Transgenomic, Gaithersburg, MD, 20878, USA). BioTechniques, 36(4), 702-704,706-707 (English) 2004. CODEN: BTNQDO. ISSN: 0736-6205. Publisher: Eaton Publishing Co..

AB A simple and flexible mutation detection technol. was developed for the discovery and mapping of both known and unknown mutations. This technol. is based on a new mismatch-specific DNA endonuclease from **celery** , Surveyor nuclease, which is a member of the CEL nuclease family of plant DNA endonucleases. Surveyor nuclease cleaves with high specificity at the 3' side of any mismatch site in both DNA strands, including all base substitutions and insertion/deletions up to at least 12 nucleotides. Surveyor nuclease technol. involves four steps: (i) PCR to amplify target DNA from both mutant and wild-type reference DNA; (ii) hybridization to form heteroduplexes between mutant and wild-type reference DNA; (iii) treatment of annealed DNA with Surveyor nuclease to cleave heteroduplexes; and (iv) anal. of digested DNA products using the detection/separation platform of choice. The technol. is highly sensitive, detecting rare mutants present at as low as 1 in 32 copies. Unlabeled Surveyor nuclease digestion products can be analyzed using conventional gel electrophoresis or high-performance liquid chromatog. (HPLC), while end-labeled digestion products are suitable for anal. by automated gel or capillary electrophoresis. The entire protocol can be performed in less than a day and is suitable for automated and high-throughput procedures.

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=> S (L13,L14) NOT L12
L27         22 ((L13 OR L14)) NOT L12

=> S L27 NOT L19
L28         22 L27 NOT L19

=> S L28 NOT L26
L29         22 L28 NOT L26

=> D 1-22 CBIB ABS
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L29 ANSWER 1 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2006:103385 Method for producing highly sensitive **endonucleases**, testing of mismatch-specific **endonucleases** and uses for detecting mismatches. Bendahmane, Abdelhafid; Sturbois, Benedicte; Triques, Karine; Caboche, Michel (Genoplante-Valor, Fr.; Institut National De La Recherche Agronomique). PCT Int. Appl. WO 2006010646 A1 20060202, 52 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR,

BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IS, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2005-EP9220 20050729. PRIORITY: WO 2004-EP9159 20040730; WO 2004-EP9166 20040730.

AB The present invention pertains to methods for producing recombinant **endonucleases** having a high sensitivity, as well as to **endonucleases** prepns. obtained by said methods, and uses thereof, especially for the detection of mismatches. The instant invention provides a simple and rapid method to obtain great quantities of **endonucleases**, in particular S1/P1 nucleases, from a small quantity of starting material, and also provides a method for evaluating the activity in vitro of candidate **endonucleases**, in particular in order to identify mismatch specific **endonucleases**. The candidate **endonucleases** that can be tested by the methods of the invention, can be found among those of the S1/P1 family. The present invention will be further illustrated by the addnl. description which follows, which refers to examples illustrating the preparation and properties of recombinant **CEL-I endonuclease**, the testing of five candidate **endonucleases** from Arabidopsis thaliana, and the identification of BFN1, (hereinafter also designated as ENDO1) as a mismatch specific **endonuclease**. The inventors found that one of these **endonucleases**, which is represented in the annexed sequence listing under SEQ ID NO: 2 (the corresponding DNA sequence is represented under SEQ ID NO: 1), and which corresponds to BFN1 of Arabidopsis thaliana, has a different specificity, and a far greater sensitivity than **CEL I**. This discovery of the properties of BFN1 as a mismatch-specific **endonuclease**, which were unknown until now, allows to propose its use as a mutation detecting reagent, for detecting mismatches resulting from base substitutions, as well as from insertion/deletions of one or more nucleotides.

L29 ANSWER 2 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN

2005:964695 Comparison of PCR-based mutation detection methods and application for identification of mouse Sult1a1 mutant embryonic stem cell clones using pooled templates. Greber, Boris; Tandara, Helena; Lehrach, Hans; Himmelbauer, Heinz (Max-Planck-Institute of Molecular Genetics, Berlin, Germany). Human Mutation, 25(5), 483-490 (English) 2005. CODEN: HUMUE3.

ISSN: 1059-7794. Publisher: Wiley-Liss, Inc..

AB Reverse genetic approaches to generate mutants of model species are useful tools to assess functions of unknown genes. Recent work has demonstrated the feasibility of such strategies in several organisms, exploiting the power of chemical mutagenesis to disrupt genes randomly throughout the genome. To increase the throughput of gene-driven mutant identification, efficient mutation screening protocols are needed. Given the availability of sequence information for large nos. of unknown genes in many species, mutation detection protocols are preferably based on PCR. Using a set of defined mutations in the Hprt1 gene of mouse embryonic stem (ES) cells, we have systematically compared several PCR-based point mutation and deletion detection methods available for their ability to identify lesions in pooled samples, which is a major

criterion for an efficient large-scale mutation screening assay. Results indicate that point mutations are most effectively identified by heteroduplex cleavage using **CEL I endonuclease.** Small deletions can most effectively be detected employing the recently described "poison" primer PCR technique. Further, we employed the **CEL I** assay followed by conventional agarose gel electrophoresis anal. for screening a library of chemical mutagenized ES cell clones. This resulted in the isolation of several clones harboring mutations in the mouse Sult1a1 locus, demonstrating the high-throughput compatibility of this approach using simple and inexpensive laboratory equipment.

L29 ANSWER 3 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2005:903015 Document No. 143:242976 Method for enriching a chemical library
synthesized on oligonucleotide templates by target binding, hybridization
and selection of homoduplexes. Freskaard, Per-Ola; Lundorf, Mikkel Dybro;
Franch, Thomas (Nuevolution A/S, Den.). PCT Int. Appl. WO 2005078122 A2 20050825, 174 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA,
BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IS, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2005-DK106 20050217. PRIORITY: DK 2004-240 20040217; US 2004-2004/PV544343 20040217.

AB A single step method of screening a chemical library for mols. binding to a specific target is described. The method uses a library synthesized using a nucleic acid template leaving the compound attached to the template. After the mol. is allowed to interact with the target, the unbound materials are eluted. The bound mols. are then identified by their nucleic acid templates. The sample is mixed with a nucleic acid probe population and hybridized to the bound templates. Heteroduplexes forming base mismatches can be selectively removed from the hybridization by degradation and homoduplexes can detected and characterized, e.g. by amplification. As the sequence is a template, identifying it also identifies the mol. it encodes.

L29 ANSWER 4 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2005:424663 Document No. 143:360652 Target-selected mutant screen by TILLING
in Drosophila. Winkler, Sylke; Schwabedissen, Anja; Backasch, Dana; Boekel, Christian; Seidel, Claudia; Boenisch, Stefanie; Fuerthauer, Maximilian; Kuhrs, Antje; Cobreros, Laura; Brand, Michael; Gonzalez-Gaitan, Marcos (Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, 01307, Germany). Genome Research, 15(5), 718-723 (English) 2005. CODEN: GEREFS. ISSN: 1088-9051. Publisher: Cold Spring
Harbor Laboratory Press.

AB The availability of the full Drosophila genomic DNA sequence prompts the development of a method to efficiently obtain mutations in genes of

interest identified by their sequence homologies or biochem. To date, molecularly characterized mutations have been generated in around 6000 of the .apprx.15,000 annotated fly genes, of which around one-third are essential for viability. To obtain mutations in essential and nonessential genes of interest, we took a reverse genetics approach, based on the large-scale detection of point mutations by **Cel-I** -mediated heteroduplex cleavage. A library of genomic DNA from 2086 EMS-mutagenized lines was established. The library was screened for mutations in three genes. A total of 6.1 Mb were screened, and 44 hits were found in two different mutagenesis conditions. Optimal conditions yielded an average of one mutation every 156 kb. For an essential gene tested, five of 25 mutations turned out to cause lethality, confirming that EMS mutagenesis leads to high frequency of gene inactivation. We thereby established that **Cel-I**-mediated TILLING can be used to efficiently obtain mutations in genes of interest in Drosophila.

L29 ANSWER 5 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2005:415275 Document No. 143:360507 TILLING moves beyond functional genomics
into crop improvement. Slade, Ann J.; Knauf, Vic C. (Anawah Inc., Seattle, WA, 98104, USA). Transgenic Research, 14(2), 109-115 (English) 2005. CODEN: TRSEES. ISSN: 0962-8819. Publisher: Springer.

AB A review. Transgenic methods have been successfully applied to trait improvement in a number of crops. However, reverse genetics studies by transgenic means are not practical in many com. important crops, hampering investigations into gene function and the development of novel and improved cultivars. A nontransgenic method for reverse genetics called Targeting Induced Local Lesions IN Genomes (TILLING) has been developed as a method for inducing and identifying novel genetic variation, and has been demonstrated in the model plant, Arabidopsis thaliana. Recently, TILLING has been extended to the improvement of crop plants and shows great promise as a general method for both functional genomics and modulation of key traits in diverse crops.

L29 ANSWER 6 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2004:802859 Document No. 141:313668 Nucleic acid template-directed synthesis
of small molecule libraries. Franch, Thomas; Jacobsen, Soeren Nyboe; Rasmussen, Torben; Neve, Soeren; Pedersen, Henrik; Gouliaev, Alex Haahr (Nuevolution A/S, Den.). PCT Int. Appl. WO 2004083427 A2 20040930, 127 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2004-DK195 20040322. PRIORITY: DK 2003-430 20030320; US 2003-2003/PV455858 20030320.

AB The method of nucleic acid template-directed synthesis of small mols. is improved. In the prior art process comprises (a) providing a nucleic acid template containing a plurality of codons and a plurality of building blocks consisting of anticodons and a reactive chemical entity, (b) hybridizing the template and building blocks, and (c) reacting the

chemical entities, under hybridization conditions, to form a product. Reactions of the chemical entities are restricted to hybridization conditions, which generally means aqueous solvents, moderate pH, and ambient temperature The improvement of the invention comprises adding a step between (b) and (c), i.e., ligating the codons to form a single-stranded oligonucleotide containing unreacted chemical entities. The chemical entities may now be reacted under any suitable conditions. In another aspect of the invention, a template is not involved, but building block oligonucleotides are capable of hybridizing to each other, or to a connector oligonucleotides.

L29 ANSWER 7 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2004:701706 Document No. 141:220876 Method for isolation of Apium graveolens
CEL II endonuclease and use for detection of
DNA mismatch. Gerard, Gary F.; Shandilya, Harini; Qiu, Peter; D'Alessio,
James M. (USA). U.S. Pat. Appl. Publ. US 2004166510 A1 20040826, 18 pp. (English). CODEN: USXXCO. APPLICATION: US 2003-688665 20031017.
PRIORITY: US 2002-PV419568 20021018.
AB The present invention relates to the isolation and characterization of **CEL I** and **CEL II**
endonuclease proteins. Methods and kits for identifying mismatches in double-stranded DNA are also provided.

L29 ANSWER 8 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2004:634059 Document No. 141:168943 Selection of perfectly matched hairpin loop structures in PCR for minimization of errors and the detection of single nucleotide polymorphisms. Makrigiorgos, G. Mike (Dana-Farber Cancer Institute, Inc., USA). PCT Int. Appl. WO 2004065582 A2 20040805, 64 pp. DESIGNATED STATES: W: AE, AE, AG, AL, AL, AM, AM, AM, AT, AT, AU,
AZ, AZ, BA, BB, BG, BG, BR, BR, BW, BY, BY, BZ, BZ, CA, CH, CN, CN, CO, CO, CR, CR, CU, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EC, EC, EE, EE, EG, ES, ES, FI, FI, GB, GD, GE, GE, GH, GM, HR, HR, HU, HU, ID, IL, IN, IS, JP, JP, KE, KE, KG, KG, KP, KP, KP, KR, KR, KZ, KZ, KZ, LC, LK, LR, LS, LS, LT, LU, LV, MA, MD, MD, MG, MK, MN, MW, MX, MX, MZ, MZ, NA, NI. (English). CODEN: PIXXD2. APPLICATION: WO 2004-US983 20040115.
PRIORITY: US 2003-2003/PV440184 20030115.
AB A method of amplifying hairpin-loop structures in DNA by PCR that allows selection of perfectly matched structures over mismatched structures arising from errors introduced by PCR is described. The method involves converting a sequence to a hairpin loop structure by ligating it with a capping oligonucleotide and a pair of oligonucleotide linkers used as primer binding sites are ligated at the ends of the sequence. Conditions are selected to allow amplification of the hairpin loop and both strands of the uncapped sequence in a single pass. When misincorporation occurs during amplification, it can be distinguished from genuine mutations that remain fully matched. Error-free DNA can be isolated by methods including denaturing HPLC, denaturing gradient gel electrophoresis, or enzymic degradation of mismatched sequences.

L29 ANSWER 9 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2004:553666 Document No. 141:200849 Genetic identity of clones and methods

to explore DNA. De Montera, B.; Boulanger, L.; Taourit, S.; Renard, J.-P.; Eggen, A. (Unite de Biologie du Developpement et Reproduction, INRA, Jouy-en-Josas, 78 352, Fr.). Cloning and Stem Cells, 6(2), 133-139
(English) 2004. CODEN: CSCLBO. ISSN: 1536-2302. Publisher: Mary Ann Liebert, Inc..

AB Cloning by nuclear transfer has made it possible to produce genetically identical animals in terms of nuclear DNA content. Recent mol. biol. tools are offering scientific ways to get an insight into the identity issues, by exploring and comparing genomes of cloned animals in order to test their genetic identity and methylation differences. Authors have initiated a study to compare genomic DNA of bovine adult clones, of normal phenotype. They have used, in parallel, the AFLP technique (amplification fragment length polymorphism) and one of its variant, MSAP (methylation-sensitive amplification polymorphism). Other techniques were also investigated leading to the detection of sequence polymorphisms between two genomes based on genomes hybridization. Authors chose the representational difference anal. (RDA) methods that can be combined with mismatch-specific recognition or mismatch binding property of some proteins (**CEL I**, MutS). Authors planned to use these RDA methods for genome-wide detection of subtle mutations, then to focus on changes affecting the methylation status of promoting genomic regions in abnormal clones. This will be achieved using MSAP with NotI and applying, in parallel, the RLGS (restriction landmark genome scanning) technique. This study will hopefully improve the mol. and functional characterizations of these "new animals".

L29 ANSWER 10 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2004:355074 Document No. 140:352649 Protein and cDNA sequences of a mutated
Apium graveolens **CEL-I-endonuclease**. Baron, Udo; Imhoff, Ulrike; Koch, Juergen; Leuer, Marco; Weber, Juergen; Olek, Klaus (Biopsytec Analytik G.m.b.H., Germany). PCT Int. Appl. WO 2004035771 A1 20040429, 36 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT,
AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2003-EP11210 20031009. PRIORITY: DE 2002-10248258 20021016.

AB The invention relates to a method for producing a recombinant, complete **CEL I**-protein, a plant **endonuclease**, and of parts thereof, by the expression of synthetic DNA-sequences. The invention also provides protein and cDNA sequences of a mutated Apium graveolens **CEL-I-endonuclease**. Moreover, the invention relates to the use of the recombinantly produced **CEL I**-enzyme for detecting point mutations as well as larger mutated regions like e.g. deletions/insertions.

L29 ANSWER 11 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2004:278664 Document No. 140:418692 Efficient discovery of DNA polymorphisms

in natural populations by ecotilling. Comai, Luca; Young, Kim; Till, Bradley J.; Reynolds, Steven H.; Greene, Elizabeth A.; Codomo, Christine A.; Enns, Linda C.; Johnson, Jessica E.; Burtner, Chris; Odden, Anthony R.; Henikoff, Steven (Department of Biology, University of Washington, Seattle, WA, 98195, USA). Plant Journal, 37(5), 778-786 (English) 2004. CODEN: PLJUED. ISSN: 0960-7412. Publisher: Blackwell Publishing Ltd..

AB We have adapted the mutation detection technol. used in Targeting Induced Local Lesions in Genomes (TILLING) to the discovery of polymorphisms in natural populations. The genomic DNA of a queried individual is mixed with a reference DNA and used to amplify a target 1-kbp region of DNA with asym. labeled fluorescent primers. After heating and annealing, heteroduplexes are nicked at mismatched sites by the **endonuclease CEL I** and cut strands are visualized using Li-cor gel analyzers. Putative polymorphisms detected in one fluorescence channel can be verified by appearance of the opposite cut strand in the other channel. We demonstrated the efficiency of this technol., called Ecotilling, by the discovery in 150+ individuals of 55 haplotypes in five genes, ranging from sequences differing by a single nucleotide polymorphism to those representing complex haplotypes. The discovered polymorphisms were confirmed by sequencing and included base-pair changes, small insertions and deletions, and variation in microsatellite repeat number Ecotilling allows the rapid detection of variation in many individuals and is cost effective because only one individual for each haplotype needs to be sequenced. The technol. is applicable to any organism including those that are heterozygous and polyploid.

L29 ANSWER 12 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN

2003:982800 Document No. 140:158127 Efficient target-selected mutagenesis in

Zebrafish. Wienholds, Erno; van Eeden, Freek; Kosters, Marit; Mudde, Josine; Plasterk, Ronald H. A.; Cuppen, Edwin (Hubrecht Laboratory, The Netherlands Institute for Developmental Biology, Utrecht, 3584 CT, Neth.).

Genome Research, 13(12), 2700-2707 (English) 2003. CODEN: GEREFS. ISSN:

1088-9051. Publisher: Cold Spring Harbor Laboratory Press.

AB One of the most powerful methods available to assign function to a gene is to inactivate or knockout the gene. Recently, the authors described the first target-selected knockout in zebrafish. Here, the authors report on the further improvements of this procedure, resulting in a highly efficient and easy method to do target-selected mutagenesis in zebrafish. A library of 4608 ENU-mutagenized F1 animals was generated and kept as a living stock. The DNA of these animals was screened for mutations in 16 genes by use of **CEL-I**-mediated heteroduplex cleavage (TILLING) and subsequent resequencing. In total, 255 mutations were identified, of which 14 resulted in a premature stop codon, 7 in a splice donor/acceptor site mutation, and 119 in an amino acid change. By this method, the authors potentially knocked out 13 different genes in a few months time. Furthermore, the authors show that TILLING can be used to detect the full spectrum of ENU-induced mutations in a vertebrate genome with the presence of many naturally occurring polymorphisms.

L29 ANSWER 13 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN

2003:819245 Document No. 140:369472 Rapid separation and laser-induced

fluorescence detection of mutated DNA by capillary electrophoresis in a self-coating, low-viscosity polymer matrix. Du, Ming; Flanagan, James H., Jr.; Lin, Bingcheng; Ma, Yinfa (Department of Chemistry, University of Missouri-Rolla, Rolla, MO, USA). Electrophoresis, 24(18), 3147-3153 (English) 2003. CODEN: ELCTDN. ISSN: 0173-0835. Publisher: Wiley-VCH Verlag GmbH & Co. KGaA.

AB The detection of point and other simple mutations in DNA is important for cancer research and diagnosis and other biol. studies. Capillary electrophoresis has been successfully used for separating DNA fragments. However, a low-viscosity polymer sieving buffer for DNA separation with online coating has never been reported. In this paper, a new method using capillary electrophoresis with online coating and laser-induced fluorescence detection (CE-LIF) for screening for point or simple DNA mutations has been demonstrated. The method uses an online dynamic coating technique that increases capillary lifetime and anal. reproducibility, and employs a low-viscosity polymer solution, which allows the user to rinse the capillary rapidly and refill with polymer solution easily. Expts. proved that the additives in the separation buffer for online capillary coating do not affect the separation efficiency of the running buffer, and do not interfere with the formation of hydrogen-bonded network between boric acid, mannitol and hydroxypropylmethylcellulose polymers. The stability of the dynamically coated capillary was quant. studied; the capillary lifetime was increased 6- to 7-fold compared with that of permanently coated CE columns. Standard DNA fragments containing mutations, with sizes of 209, 219, and 338 bps, were successfully separated and detected with this system, after the mutated DNA fragments were cleaved by **CEL -I endonuclease**. The technique is very sensitive for the size-separation of low-range, middle-range, and high-range DNA fragments. Results were compared with the HPLC methods developed by Transgenomic, Inc. and were in good agreement. The method should be applicable to mutation detection for all relevant biol. and clin. studies. The factors influencing sepns. and the stability of dynamic capillary coatings are also discussed in the paper.

L29 ANSWER 14 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN

2003:740342 Document No. 139:359418 High-throughput TILLING for functional genomics. Till, Bradley J.; Colbert, Trenton; Tompa, Rachel; Enns, Linda C.; Codomo, Christine A.; Johnson, Jessica E.; Reynolds, Steven H.; Henikoff, Jorja G.; Greene, Elizabeth A.; Steine, Michael N.; Comai, Luca; Henikoff, Steven (Basic Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA, USA). Methods in Molecular Biology (Totowa, NJ, United States), 236(Plant Functional Genomics), 205-220 (English) 2003. CODEN: MMBIED. ISSN: 1064-3745. Publisher: Humana Press Inc..

AB Targeting-induced local lesions in genomes (TILLING) is a general strategy for identifying induced point mutations that can be applied to almost any organism. Here, we describe the basic methodol. for high-throughput TILLING. Gene segments are amplified using fluorescently tagged primers, and products are denatured and reannealed to form heteroduplexes between the mutated sequence and its wild-type counterpart. These heteroduplexes are substrates for cleavage by the **endonuclease CEL I**. Following cleavage, products are analyzed on

denaturing polyacrylamide gels using the LI-COR DNA analyzer system. High-throughput TILLING has been adopted by the Arabidopsis TILLING Project (ATP) to provide allelic series of point mutations for the general Arabidopsis community.

L29 ANSWER 15 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2003:656327 Document No. 139:192439 Selaginella lepidophylla **endonuclease CEL I** and RES I, and use for detecting mismatch and single nucleotide polymorphisms. Padgett, Hal S.; Vaewhongs, Andrew A.; Vojdani, Fakhrieh S.; Smith, Mark L.; Lindbo, John A.; Fitzmaurice, Wayne P. (USA). U.S. Pat. Appl. Publ. US 2003157682 A1 20030821, 79 pp., Cont.-in-part of U.S. Ser. No. 211,079. (English). CODEN: USXXCO. APPLICATION: US 2003-356708 20030131. PRIORITY: US 2002-2002/PV35372U 20020201; US 2002-2002/98155 20020314; US 2002-2002/211079 20020801.

AB The invention provides Selaginella lepidophylla restriction **endonuclease CEL I** and RES I. Restriction **endonucleases** are useful in finding single nucleotide polymorphisms. They are also useful in an in vitro method of redistributing sequence variations between non-identical polynucleotide sequences.

L29 ANSWER 16 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2003:454522 Document No. 139:18346 Methods for the selection and cloning of nucleic acid molecules free of unwanted mutations. Lok, Si; Tannheimer, Stacey (Zymogenetics, Inc., USA). PCT Int. Appl. WO 2003048395 A1 20030612, 29 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-US38467 20021203. PRIORITY: US 2001-2001/PV336888 20011203.

AB The accurate synthesis of nucleic acid mols. is important for use of amplified nucleic acid mols. as hybridization probes, in the regulation of gene expression, as templates for the production of recombinant proteins, as diagnostic probes, and in forensic analyses. Methods are provided to sep. nucleic acid mols. that are free of mutations from a population of nucleic acid mols. that contain unwanted nucleotide alternations.

L29 ANSWER 17 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2002:76606 Document No. 137:75078 High-Throughput Analysis of Nucleic Acid Modification Reactions Using Ion-Pair Reverse-Phase High-Performance Liquid Chromatography. Dickman, Mark J.; Matin, Maryam M.; Hornby, David P. (Transgenomic Research Laboratory, Krebs Institute, University of Sheffield, Sheffield, S10 2TN, UK). Analytical Biochemistry, 301(2), 290-297 (English) 2002. CODEN: ANBCA2. ISSN: 0003-2697. Publisher: Academic Press.

AB Ion-pair reverse-phase high-performance liquid chromatog. is presented as a versatile platform for the rapid anal. of nucleic acid modification reactions in a high-throughput manner. This system allows both sensitive and nonradioactive assays to be developed for a variety of nucleic acid modification reactions. Examples presented here include assays for telomerase, uracil DNA glycosylase, polynucleotide kinase, T4 DNA ligase, C5-DNA methyltransferases, and the mismatch **endonuclease CEL I**. However, this approach is not confined to these reactions. Indeed the ability to perform a variety of nonradioactive assays with throughput times of 10 min per sample in conjunction with automated data anal. software represents a significant improvement in anal. and preparative nucleic acid enzymol. (c) 2002 Academic Press.

L29 ANSWER 18 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2001:909210 Document No. 136:364366 Detection of simple mutations and polymorphisms in large genomic regions. Sokurenko, Evgeni V.; Tchesnokova, Veronika; Yeung, Anthony T.; Oleykowski, Catherine A.; Trintchina, Elena; Hughes, Kelly T.; Rashid, Rebecca A.; Brint, J. Mark; Moseley, Steve L.; Lory, Stephen (Department of Microbiology, University of Washington, Seattle, WA, 98195, USA). Nucleic Acids Research, 29(22), e111/1-e111/8 (English) 2001. CODEN: NARHAD. ISSN: 0305-1048. Publisher: Oxford University Press.

AB The authors have developed a novel technol. that makes it possible to detect simple nucleotide polymorphisms directly within a sample of total genomic DNA. It allows, in a single Southern blot experiment, the determination of sequence identity of genomic regions with a combined length of hundreds of kilobases. This technol. does not require PCR amplification of the target DNA regions, but exploits preparative size-fractionation of restriction-digested genomic DNA and a newly discovered property of the mismatch-specific **endonuclease CEL I** to cleave heteroduplex DNA with a very high specificity and sensitivity. This technique was used to detect various simple mutations directly in the genomic DNA of isogenic pairs of recombinant Pseudomonas aeruginosa, Escherichia coli and Salmonella isolates. Also, a cosmid DNA library and genomic fractions as hybridization probes were used to compare total genomic DNA of two clin. P. aeruginosa clones isolated from the same patient, but exhibiting divergent phenotypes. The mutation scan correctly detected a GA insertion in the quorum-sensing regulator gene rhlR and, in addition, identified a novel intragenomic polymorphism in rrn operons, indicating very high stability of the bacterial genomes under natural non-mutator conditions.

L29 ANSWER 19 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2001:854669 Document No. 136:335606 Discovering the sweeping power of point mutations using a GIRAFF. Sokurenko, Evgeni V. (Dept. of Microbiology, University of Washington, Seattle, WA, 98195, USA). Trends in Microbiology, 9(11), 522-525 (English) 2001. CODEN: TRMIEA. ISSN: 0966-842X. Publisher: Elsevier Science Ltd..

AB A review. In pathogenic bacteria, point and other simple mutations can provide a strong selective advantage during the course of a single infection. Our understanding of the importance of these randomly occurring mutations has been hampered by a lack of technologies allowing mutation scanning on a genomic scale. Here, a novel technol. is

described that makes it possible to scan, in a single Southern blot experiment, the sequence identity of genomic regions with a combined length of hundreds of kilobases.

L29 ANSWER 20 OF 22 CAPLUS COPYRIGHT 2006 ACS on STN
2001:763236 Document No. 135:314400 Method for identifying and isolating genome fragments with linkage disequilibrium. Olek, Klaus; Weber, Juergen; Jansen, Thomas; Leuer, Marco (QTL A.-G. Gesellschaft zur Erforschung Komplexer Genetischer Merkmale, Germany). PCT Int. Appl. WO 2001077374 A2 20011018, 36 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (German). CODEN: PIXXD2. APPLICATION: WO 2001-DE1488 20010408. PRIORITY: DE 2000-10017675 20000408.

AB The invention relates to a method for identifying and isolating genome fragments with linkage disequil. For related and unrelated individuals, parts of the genome which contain candidate gene parts that are in linkage disequil. with their narrow DNA environment are isolated. The clonation step is carried out earlier than in other methods, enabling the DNA fragments to be obtained independently of volume and also replacing the methylation step still carried out in other methods. The inventive use of a plant enzyme considerably increases the specificity of the inventive method compared to methods which use the mut S,H,L complex.

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2001:748055 Document No. 135:283948 Reverse genetic strategy for identifying functional mutations, TILLING (targeting induced local lesions in genomics) that combines chemical mutagenesis with a sensitive mutation detection. McCallum, Claire M.; Henikoff, Steven; Colbert, Trenton (Fred Hutchinson Cancer Research Center, USA). PCT Int. Appl. WO 2001075167 A1 20011011, 57 pp. DESIGNATED STATES: W: AU, CA, JP, US; RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2001-US10545 20010330. PRIORITY: US 2000-PV193794 20000331.

AB The present invention provides a reverse genetic method for identifying functional mutations in a gene of known sequence comprising treating an organism or cell with mutagen which induces mutations in the DNA of an organism or cell; preparing isolated genomic DNA from the mutagenized organism or cell; amplifying a region of a gene of known sequence; and screening for mutations in the mutagenized DNA sequence in the gene as compared to the same sequence of the gene in the wild type parent organism or cell. The method designated TILLING, for Targeted Induced Local Lesion in Genomes, combines the high d. of mutations provided by traditional mutagenesis methods with rapid mutational anal. methods to identify mutations of interest in genes of known sequence without

inserting heterologous nucleic acids into an organism or cell. Samples, of the mutagenized organism or cells are then collected and DNA samples are pooled for anal. by nucleic acid amplification, heteroduplex anal. to determine the approx. location of the mutation, and optionally DNA sequencing. In TILLING the mutations detected are either missense or nonsense mutations which result in altered or truncated protein products. The organisms or cells analyzed by the disclosed methods can be either homozygous or heterozygous for the mutation of interest. The methods of the present invention are applicable to any organism which can be heavily mutagenized, including both plants and animals. In a specific embodiment, TILLING has been applied to two Arabidopsis thaliana chromomethylase genes related to CMT 1, a DNA methyltransferase homolog with a chromodomain (Henikoff and Comai, Genetics 149:307-318 (1998)). A new reverse genetic strategy for introducing mutations in plants is introduced that combines the high d. of point mutations provided by traditional chemical mutagenesis with rapid mutational screening to discover induced lesions. TILLING (targeting induced local lesions in genomics) combines chemical mutagenesis with a sensitive mutation detection instrument. In a pilot experiment, DNA from a collection of EMS-mutagenized Arabidopsis plants was pooled, subjected to PCR amplification, and screening for mutations using denaturing HPLC. Among the lesions detected were base transitions causing missense and nonsense changes that can be used for phenotypic analyses. TILLING is suitable for any organism that can be heavily mutagenized, even those that lack genetic tools.

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2001:465489 Document No. 136:129593 High-throughput screening for induced point mutations. Colbert, Trenton; Till, Bradley J.; Tompa, Rachel; Reynolds, Steve; Steine, Michael N.; Yeung, Anthony T.; McCallum, Claire M.; Comai, Luca; Henikoff, Steven (Basic Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA, 98109, USA). Plant Physiology, 126(2), 480-484 (English) 2001. CODEN: PLPHAY. ISSN: 0032-0889. Publisher: American Society of Plant Physiologists.

AB The targeting induced local lesions in genomes (TILLING) reverse genetic strategy was modified to suit the large-scale screening of chemical induced mutations in Arabidopsis and other plants. In the new high-throughput screening method, amplification products are incubated with an **endonuclease** that preferentially cleaves mismatches in heteroduplexes between wild type and mutant. Cleavage products are electrophoresed using an automated sequencing gel apparatus, and gel images are analyzed with the aid of a standard com. image processing program. Upon detection of a mutation in a pool, the individual DNA samples are similarly screened to identify the plant carrying the mutation. This rapid screening procedure dets. the location of a mutation to within a few base pairs for PCR products up to 1 kb in size. The new method takes advantage of robust equipment developed for high-throughput sequencing and genotyping and a popular image anal. program to streamline plant reverse genetics.

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=> FILE CAPLUS

=> S HEPARIN
         46702 HEPARIN
          1796 HEPARINS
L1        46817 HEPARIN
                (HEPARIN OR HEPARINS)

=> S CEL I;S CEL II;S ENDONUCLEASE;S NUCLEASE
          2294 CEL
           165 CELS
          2428 CEL
                (CEL OR CELS)
       4161362 I
L2           54 CEL I
                (CEL(W)I)


          2294 CEL
           165 CELS
          2428 CEL
                (CEL OR CELS)
       2069105 II
           895 IIS
       2069615 II
                (II OR IIS)
L3           21 CEL II
                (CEL(W)II)


         27561 ENDONUCLEASE
          8226 ENDONUCLEASES
L4        31976 ENDONUCLEASE
                (ENDONUCLEASE OR ENDONUCLEASES)


         20902 NUCLEASE
          6307 NUCLEASES
L5        25079 NUCLEASE
                (NUCLEASE OR NUCLEASES)

=> S L1 AND (L2,L3)
L6            1 L1 AND ((L2 OR L3))

=> D CBIB ABS

L6   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2006 ACS on STN
2004:701706   Document No. 141:220876  Method for isolation of Apium graveolens
     CEL II endonuclease and use for detection of DNA
     mismatch.  Gerard, Gary F.; Shandilya, Harini; Qiu, Peter; D'Alessio,
     James M. (USA).  U.S. Pat. Appl. Publ. US 2004166510 A1 20040826, 18 pp.
     (English).  CODEN: USXXCO.  APPLICATION: US 2003-688665 20031017.
     PRIORITY: US 2002-PV419568 20021018.
AB   The present invention relates to the isolation and characterization of CEL I and
     CEL II endonuclease
     proteins.  Methods and kits for identifying mismatches in double-stranded DNA are
     also provided.
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	L #	Hits	Search Text	DBs
1	L1	38	CEL ADJ I	US-PGPUB; USPAT
2	L2	30	CEL ADJ II	US-PGPUB; USPAT
3	L3	38678	HEPARIN	US-PGPUB; USPAT
4	L4	4	L3 AND (L1 OR L2)	US-PGPUB; USPAT
5	L5	3	L1 SAME L2	US-PGPUB; USPAT
6	L6	2663918	SEPARAT$	US-PGPUB; USPAT
7	L7	61	L6 AND (L1 OR L2)	US-PGPUB; USPAT
8	L8	17	L6 SAME (L1 OR L2)	US-PGPUB; USPAT